

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 27.1047 Seconds
(Without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613b-21

Perfect score: 603

Sequence: 1 MGNMATEFOOKHIINTPIICN.....ICVKEENQYVHFAGIGRCP 111

Scoring table: BLDSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_21:*

- 1: sp._archaea:*
- 2: sp._bacteria:*
- 3: sp._fungi:*
- 4: sp._human:*
- 5: sp._invertebrate:*
- 6: sp._mammal:*
- 7: sp._mhc:*
- 8: sp._organelle:*
- 9: sp._phage:*
- 10: sp._plant:*
- 11: sp._rodent:*
- 12: sp._virus:*
- 13: sp._vertebrate:*
- 14: sp._unclassified:*
- 15: sp._viral:*
- 16: sp._bacteriophage:*
- 17: sp._archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585.5	96.8	133	13	09PMW7 rana catesb
2	554.5	91.7	133	13	09SMO rana catesb
3	483.5	79.9	132	13	09SM2 rana catesb
4	474.5	78.4	133	13	09SM19 rana catesb
5	467.5	77.3	133	13	09SM18 rana catesb
6	444.5	73.5	132	13	09SM1 rana catesb
7	372	61.5	132	13	09SM78 rana catesb
8	277.5	45.9	137	13	09SM8 rana catesb
9	273.5	45.2	127	13	08UVX5 rana pipien
10	243	40.2	129	13	08UVX5 rana pipien
11	225.5	37.3	128	13	09DFY8 rana catesb
12	223.5	36.9	128	13	09DFY7 rana catesb
13	214.5	35.5	128	13	09DFY5 rana catesb
14	161	26.6	169	13	09W738 xenopus lae
15	128	21.2	170	6	09BEC1 traagulus ja
16	121.5	20.1	116	6	09TWC0 sus scrofa

17	121.5	20.1	163	6	09BDC2	09BDC2 antilocapra
18	121	20.0	150	11	08VD94	08VD94 beryllus bo
19	119	19.7	150	11	08VD88	08VD88 rattus norv
20	118.5	19.6	144	6	09BH14	09BH14 antilocapra
21	116	19.2	150	11	08VD92	08VD92 rattus exul
22	113.5	18.8	152	11	08VD89	08VD89 rattus norv
23	112.5	18.6	119	6	09TV33	09TV33 bos taurus
24	110.5	18.3	124	6	09SNE6	09SNE6 bubalus bub
25	109.5	18.1	149	11	08VD95	08VD95 beryllus bo
26	109	18.0	124	6	09BEC2	09BEC2 traagulus ja
27	109	18.0	134	6	09BDB9	09BDB9 traagulus ja
28	108.5	17.9	152	11	08VD84	08VD84 rattus liom
29	108.5	17.9	156	6	08S005	08S005 lagotrichix l
30	107.5	17.8	119	6	09TV30	09TV30 sagunus oe
31	107.5	17.8	119	6	09TV28	09TV28 eulemur ful
32	106.5	17.6	124	6	09TSF2	09TSF2 bos taurus
33	106.5	17.6	156	6	08S006	08S006 ateles geof
34	105.5	17.4	142	6	09BEC3	09BEC3 traagulus ja
35	105.5	17.4	156	6	08S008	08S008 salmifri sci
36	105.5	17.4	156	6	08S007	08S007 sagunus oe
37	104.5	17.3	152	11	08VD90	08VD90 rattus fusc
38	103.5	17.1	116	6	09T933	09T933 phococenoide
39	103.5	17.1	119	11	08VD93	08VD93 rattus exul
40	102.5	16.9	116	6	09T934	09T934 pseudorca c
41	102.5	16.9	119	6	09TS06	09TS06 cercopithec
42	101.5	16.8	119	6	09TV32	09TV32 gorilla gor
43	101.5	16.8	124	6	09XS40	09XS40 camelus bac
44	101.5	16.8	157	11	09JKJ4	09JKJ4 meriones un
45	101.5	16.8	158	6	08SPY3	08SPY3 sagunus la

ALIGNMENTS

RESULT 1	ID	Q9PMW7	PRELIMINARY	PRT:	133 AA.
AC	Q9PMW7				
DT	01-MAY-2000	(TREMURel. 13, Created)			
DT	01-MAY-2000	(TREMURel. 13, Last sequence update)			
DT	01-DEC-2001	(TREMURel. 19, Last annotation update)			
DE	Ribonuclease precursor.				
GN	RCR.				
OS	Rana catesbeiana (Bull frog).				
OC	Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:				
OX	NCBI_TaxID=8400;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER.				
RX	MEDLINE=98165825; PubMed=9497370;				
RA	Huang H.C., Wang S.C., Liu Y.J., Lu S.C., Liao Y.D.;				
RT	"The Rana catesbeiana rcr gene encoding a cytototoxic ribonuclease.				
RT	Tissue distribution, cloning, purification, cytotoxicity, and active				
RL	residues for RNase activity."				
RL	J. Biol. Chem. 273:6395-6401(1998).				
DR	EMBL: AF039104; AAD10702.1;				
DR	HSSP: P11916; IRCA				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; RNaseA; 1.				
DR	ProDom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase_PC; 1.				
DR	PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.				
KW	SIGNAL.				
FT	SIGNAL	1	22		POTENTIAL.
FT	CHAIN	23	133		RIBONUCLEASE.
SO	SEQUENCE	133 AA;	14762 MW;	A7D62594F7D16F0C	CRC64;
QY	Query Match	96.8%;	Score 585.5;	DB 13;	Length 133;
	Best Local Similarity	97.3%;	Pred. No. 6.6e-60;		
	Matches 108;	Conservative 2;	Mismatches 0;	Indels 1;	Gaps 1;
					2 QNMATEFOOKHIINTPII-CMTILDNNIYVGQCKRVNTEFISSATTVAIKICGVINLVN 60

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Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 133

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RESULT 2

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O98SMO ID Q98SMO PRELIMINARY: PRT: 133 AA.

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AC Q98SMO: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_TaxID=8400;

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RP SEQUENCE FROM N.A.

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RX MEDLINE=21539506; PubMed=11683320;

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RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

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RT "Rapid diversification of RNase A superfamily ribonuclease from the

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RL J. Mol. Evol. 53:31-38(2001).

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DR EMBL: AF351209; AAK30255.1;

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DR HSSP: P11916; IBC4.

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DR InterPro: IPR001427; RNaseA.

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DR Pfam: PF00074; RNaseA.1.

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DR ProDom: PD000535; RNaseA.1.

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DR SMART: SM00092; RNase_Pc.1.

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DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.

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KW Signal.

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FT SIGNAL 1 22 POTENTIAL.

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SQ SEQUENCE 133 AA: 14628 MW: 87FCF122C3499E02 CRC64;

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Query Match Best Local Similarity 91.7%; Score 554.5; DB 13; Length 133;

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Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

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Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 133

```

RESULT 3

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O98SM2 ID Q98SM2 PRELIMINARY: PRT: 132 AA.

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AC Q98SM2: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_TaxID=8400;

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RP SEQUENCE FROM N.A.

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```

RX MEDLINE=21539506; PubMed=11683320;

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```

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

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```

RT "Rapid diversification of RNase A superfamily ribonuclease from the

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```

RL J. Mol. Evol. 53:31-38(2001).

```

```

KW Signal.

```

```

FT SIGNAL 1 22 POTENTIAL.

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```

SQ SEQUENCE FROM N.A.

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RC TISSUE=LIVER;

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```

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;

```

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RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF351207; AAK30253.1;

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DR EMBL: AF359578; AAL87036.1;

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DR HSSP: P11916; IBC4.

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DR InterPro: IPR001427; RNaseA.

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DR Pfam: PF00074; RNaseA.1.

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DR ProDom: PD000535; RNaseA.1.

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DR SMART: SM00092; RNase_Pc.1.

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DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.

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KW Signal.

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FT SIGNAL 1 22 POTENTIAL.

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FT CHAIN 23 132 RC-RNASE7.

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SQ SEQUENCE 132 AA: 14412 MW: 131A745187978687 CRC64;

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Query Match Best Local Similarity 79.9%; Score 483.5; DB 13; Length 132;

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Matches 91; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

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Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 110
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 132

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RESULT 4

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O98SL9 ID Q98SL9 PRELIMINARY: PRT: 133 AA.

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AC Q98SL9: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_TaxID=8400;

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RP SEQUENCE FROM N.A.

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RX MEDLINE=21539506; PubMed=11683320;

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```

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

```

```

RT "Rapid diversification of RNase A superfamily ribonuclease from the

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RL J. Mol. Evol. 53:31-38(2001).

```

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DR EMBL: AF351210; AAK30256.1;

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DR HSSP: P11916; IBC4.

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DR InterPro: IPR001427; RNaseA.

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DR Pfam: PF00074; RNaseA.1.

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DR ProDom: PD000535; RNaseA.1.

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DR SMART: SM00092; RNase_Pc.1.

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DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.

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KW Signal.

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FT SIGNAL 1 22 POTENTIAL.

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SQ SEQUENCE 133 AA: 14615 MW: C8785B236B26E54E CRC64;

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Query Match Best Local Similarity 78.4%; Score 474.5; DB 13; Length 133;

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Matches 86; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

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Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFAIGRCP 132

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RESULT 5

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O98SL8

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ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, *Rana catesbeiana*.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF51211; AAC30257.1; -;
DR HSSP; P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A4FA5B943 CRC64;
Query Match 77.3%; Score 467.5; DB 13; Length 133;
Best Local Similarity 75.7%; Pred. No. 2.8e-46;
Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;
QY 2 QNATFOCKHIINPPII-CNTIILNNIYVGGCKRVNTFISSATTVKATCGVILNV 60
DB 23 QNATFOCKHIITSSINCNNIMNSLYVGGCKKYNFTIASSATTVKATCGVILNV 82
QY 61 LSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 111
DB 83 LSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 133
RESULT 6
ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, *Rana catesbeiana*.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF51208; AAC30254.1; -;
DR HSSP; P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
Query Match 73.5%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 1.2e-43;

Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
QY 2 QNATFOCKHIINPPII-CNTIILNNIYVGGCKRVNTFISSATTVKATCGVILNV 60
DB 23 QNATFOCKHIITSSINCNNIMNSLYVGGCKKYNFTIASSATTVKATCGVILNV 82
QY 61 LSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 110
DB 83 LSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 132
RESULT 7
ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytochrome b ribonucleases from *Rana
RT catesbeiana* (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF288642; AAC30414.2; -;
DR HSSP; P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBE53 CRC64;
Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
QY 2 QNATFOCKHIINPPII-CNTIILNNIYVGGCKRVNTFISSATTVKATCGVILNV 59
DB 22 QNATFOCKHIITSSINCNNIMNSLYVGGCKKYNFTIASSATTVKATCGVILNV 81
QY 60 VLSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 110
DB 82 ELSTTRFQLNCTRTSTPRPCPYSSRTETNYICVCKENQVPHFAGIGRC 132
RESULT 8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
OS Rana pipiens (Northern Leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8404;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20330357; PubMed=10871370;
 RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
 RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
 RT 3 UTR of unusual length and structure."
 RL Nucleic Acids Res. 28:2375-2382(2000).
 DR EMBL; AF165133; AAF76935.1; -
 DR HSP; P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 45.9%; Score 277.5; DB 13; Length 127;
 Best Local Similarity 48.6%; Pred. No. 2.3e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 ONMATEOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59
 DB 24 QDMLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFTYSRPEPVKAICKGIIASKN 79
 QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 DB 80 VLTSEFYLSDC---NVTSRPKYKIKLKSTNFCVTCENQAPVHFVGVGCHC 127

RESULT 9

Q8UVX5 PRELIMINARY; PRT; 127 AA.
 AC Q8UVX5:

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Oncocase precursor.
 GN RPR.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8404;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AF332139; AAL54383.1; -
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 45.2%; Score 273.5; DB 13; Length 127;
 Best Local Similarity 48.6%; Pred. No. 6.6e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 ONMATEOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59
 DB 24 QDMLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFTYSRPEPVKAICKGIIASKN 79

QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 DB 80 VLTSEFYLSDC---NVTSRPKYKIKLKSTNFCVTCENQAPVHFVGVGSC 127

RESULT 10

Q9DFY6 PRELIMINARY; PRT; 129 AA.
 AC Q9DFY6:

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 RT catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR HSP; P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.2%; Score 243; DB 13; Length 129;
 Best Local Similarity 42.5%; Pred. No. 2.2e-20;
 Matches 48; Conservative 25; Mismatches 30; Indels 10; Gaps 5;

QY 2 ONMATEOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59
 DB 24 QDMLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFTYSRPEPVKAICKGIIASKN 79
 QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 111
 DB 80 VLSNSEFYLAEC---NVKPRPKYKIKLKSSNRICRCEHLPVHFAGVIGCP 129

RESULT 11

Q9DFY8 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY8:

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 RT catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR HSP; P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 128 AA; 14724 MW; 826A62882B10ABDA CRC64;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF242553; AAC31439.1; -
 DR HSSP: P22069; 10NC
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.3%; Score 225.5; DB 13; Length 128;
 Best Local Similarity 39.3%; Pred. No. 2.3e-18;
 Matches 44; Conservative 21; Mismatches 98; Indels 9; Gaps 4;

OY 2 QNATFOOKHIIINT-PIICNTIIDNNIYIGGCKRVNTFISSATVKAICTGVI-INLN 59
 DB 24 QNMTFOCKHIIITDROKCAEMKALF---DCKKNTFIYARGVQALCKNIISKV 79
 60 VLSTRQLNCTRTSTIPRCYSSRTETNYICVCKENQPVHFAIGRCP 111
 80 VLSTEEFYLLDPCNRKIL---PCHYKLRKSSNTICITCKELPIHFAVGECR 128

RESULT 12

O9DFY7 PRELIMINARY; PRT; 128 AA.
 AC O9DFY7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase3 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL: AF242554; AAC31440.2; -
 DR HSSP: P22069; 10NC
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 36.9%; Score 223.5; DB 13; Length 128;
 Best Local Similarity 40.2%; Pred. No. 4e-18;
 Matches 45; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

OY 2 QNATFOOKHIIINT-PIICNTIIDNNIYIGGCKRVNTFISSATVKAICTGV-INLN 59
 DB 24 QDMTFPOCKHIIITDPRKVCDEMKAALF---DCKKNTFIYALPGRKVALCKNIRNMTD 79
 60 VLSTRQLNCTRTSTIPRCYSSRTETNYICVCKENQPVHFAIGRCP 111
 80 VLSDNALDPCNRKIL---PCHYKLRKSSNTICITCKENQPLHFAVGECR 128

RESULT 13

O9DFY5 PRELIMINARY; PRT; 128 AA.
 AC O9DFY5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase6 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 35.5%; Score 214.5; DB 13; Length 128;
 Best Local Similarity 38.4%; Pred. No. 4.3e-17;
 Matches 43; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

RESULT 14

O9W738 PRELIMINARY; PRT; 169 AA.
 AC O9W738;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FRU2 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96069863; PubMed=7585965;
 RA Kinoshita N., Minshull J., Kirschner M.W.;
 RT "The identification of two novel ligands of the fgg receptor by a
 yeast screening method and their activity in Xenopus development.";
 RL Cell 83:621-630(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kinoshita N., Kirschner M.W.;

